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RAW SEQUENCE LISTING DATE: 10/29/2001
PATENT APPLICATION: US/09/927,850 TIME: 15:41:28

Input Set : A:\99372Fseq.txt
Output Set: N:\CRF3\10292001\I927850.raw

<110> APPLICANT: Welcher, Andrew
Wen, Duanzhi
Kelly, Michael
<120> TITLE OF INVENTION: Interferon-Like Molecules and Uses Thereof
<130> FILE REFERENCE: 99,372-F
<140> CURRENT APPLICATION NUMBER: 09/927,850
<141> CURRENT FILING DATE: 2001-08-10
<150> PRIOR APPLICATION NUMBER: 09/724,860
<151> PRIOR FILING DATE: 2000-11-28
<150> PRIOR APPLICATION NUMBER: 60/169,720
<151> PRIOR FILING DATE: 1999-12-08
<160> NUMBER OF SEQ ID NOS: 39
<170> SOFTWARE: PatentIn Ver. 2.0
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<211> LENGTH: 913
<212> TYPE: DNA
<213> ORGANISM: Rattus norvegicus
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<222> LOCATION: (53)..(625)
<220> FEATURE:
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Leu Lys Tyr Leu Trp Leu Val Ala Leu Val Ala Leu Tyr Ile Ser Pro
          5                  10                  15

atc cag tct cag aac tgt gtg tat ctg gat cat acc atc ttg gaa aac 154
Ile Gln Ser Gln Asn Cys Val Tyr Leu Asp His Thr Ile Leu Glu Asn
     20                  25                  30

atg aaa ctt ctg agc agc atc agg acc acc ttt ccc tta aga tgt cta 202
Met Lys Leu Leu Ser Ser Ile Arg Thr Thr Phe Pro Leu Arg Cys Leu
 35                  40                  45                  50

aaa gat atc acg gat ttt gag ttt cct caa gag att ctg ctg tac gtc 250
Lys Asp Ile Thr Asp Phe Glu Phe Pro Gln Glu Ile Leu Leu Tyr Val
                 55                  60                  65

cag cat gtg aaa aag gac ata aag gca gtc acc tat cat ata tct tct 298
Gln His Val Lys Lys Asp Ile Lys Ala Val Thr Tyr His Ile Ser Ser
             70                  75                  80

ctg gcg cta att att ttc agt ctt aaa gac tcc atc tcc ctg gcg aca 346
Leu Ala Leu Ile Ile Phe Ser Leu Lys Asp Ser Ile Ser Leu Ala Thr
         85                  90                  95

gag gaa cgc ttg gaa cgt atc aga tcg gga ctt ttc aaa caa gtg cag 394
Glu Glu Arg Leu Glu Arg Ile Arg Ser Gly Leu Phe Lys Gln Val Gln
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68     100                 105                 110
70 caa gct cga gag tgc atg gta gac gag gag aac aag aac acg gag gag   442
71 Gln Ala Arg Glu Cys Met Val Asp Glu Glu Asn Lys Asn Thr Glu Glu
72 115                 120                 125                 130
74 gac agt aca tca caa cat cct cac tca gag ggc ttc aag gca gtc tac   490
75 Asp Ser Thr Ser Gln His Pro His Ser Glu Gly Phe Lys Ala Val Tyr
76                 135                 140                 145
78 ctg gaa ttg aac aag tat ttc ttc aga atc aga aag ttc ctg gta aat   538
79 Leu Glu Leu Asn Lys Tyr Phe Phe Arg Ile Arg Lys Phe Leu Val Asn
80             150                 155                 160
82 aag aaa tac agt ttc tgt gcc tgg aag att gtc gtg gtg gaa ata aga   586
83 Lys Lys Tyr Ser Phe Cys Ala Trp Lys Ile Val Val Val Glu Ile Arg
84         165                 170                 175
86 aga tgt ttc agt ata ttt tac aaa cta ctc aac atg aat tgagaatcat    635
87 Arg Cys Phe Ser Ile Phe Tyr Lys Leu Leu Asn Met Asn
88     180                 185                 190
90 ccagcttcaa gcaagaactt agatagaagt tgtgactgct caaatgtccc caagaacgct 695
92 tgattctaag gctattgcga gtctgctgct acacacttcg gacgcaagac ttttcaaggt 755
94 cagggttcaa ggtagtacag tcaaaggaag tcttatgtta agcaaaagaa aaatttcagt 815
96 ggaaaagcta gcagaaatgt caacttgtca aaaaaacaac ttatggatta tggcattgac 875
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103 <212> TYPE: PRT
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111             20                  25                  30
113 Glu Asn Met Lys Leu Leu Ser Ser Ile Arg Thr Thr Phe Pro Leu Arg
114         35                  40                  45
116 Cys Leu Lys Asp Ile Thr Asp Phe Glu Phe Pro Gln Glu Ile Leu Leu
117     50                  55                  60
119 Tyr Val Gln His Val Lys Lys Asp Ile Lys Ala Val Thr Tyr His Ile
120 65                  70                  75                  80
122 Ser Ser Leu Ala Leu Ile Ile Phe Ser Leu Lys Asp Ser Ile Ser Leu
123                 85                  90                  95
125 Ala Thr Glu Glu Arg Leu Glu Arg Ile Arg Ser Gly Leu Phe Lys Gln
126             100                 105                 110
128 Val Gln Gln Ala Arg Glu Cys Met Val Asp Glu Glu Asn Lys Asn Thr
129         115                 120                 125
131 Glu Glu Asp Ser Thr Ser Gln His Pro His Ser Glu Gly Phe Lys Ala
132     130                 135                 140
134 Val Tyr Leu Glu Leu Asn Lys Tyr Phe Phe Arg Ile Arg Lys Phe Leu
135 145                 150                 155                 160
137 Val Asn Lys Lys Tyr Ser Phe Cys Ala Trp Lys Ile Val Val Val Glu
138                 165                 170                 175
140 Ile Arg Arg Cys Phe Ser Ile Phe Tyr Lys Leu Leu Asn Met Asn
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Input Set : A:\99372Fseq.txt
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151   1               5                  10                  15
153 Ser Ile Arg Thr Thr Phe Pro Leu Arg Cys Leu Lys Asp Ile Thr Asp
154              20                  25                  30
156 Phe Glu Phe Pro Gln Glu Ile Leu Leu Tyr Val Gln His Val Lys Lys
157          35                  40                  45
159 Asp Ile Lys Ala Val Thr Tyr His Ile Ser Ser Leu Ala Leu Ile Ile
160      50                  55                  60
162 Phe Ser Leu Lys Asp Ser Ile Ser Leu Ala Thr Glu Glu Arg Leu Glu
163  65                  70                  75                  80
165 Arg Ile Arg Ser Gly Leu Phe Lys Gln Val Gln Gln Ala Arg Glu Cys
166                  85                  90                  95
168 Met Val Asp Glu Glu Asn Lys Asn Thr Glu Glu Asp Ser Thr Ser Gln
169              100                 105                 110
171 His Pro His Ser Glu Gly Phe Lys Ala Val Tyr Leu Glu Leu Asn Lys
172          115                 120                 125
174 Tyr Phe Phe Arg Ile Arg Lys Phe Leu Val Asn Lys Lys Tyr Ser Phe
175      130                 135                 140
177 Cys Ala Trp Lys Ile Val Val Val Glu Ile Arg Arg Cys Phe Ser Ile
178 145                 150                 155                 160
180 Phe Tyr Lys Leu Leu Asn Met Asn
181                 165
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 1836
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
189 <220> FEATURE:
190 <221> NAME/KEY: CDS
191 <222> LOCATION: (575)..(1195)
193 <220> FEATURE:
194 <221> NAME/KEY: sig_peptide
195 <222> LOCATION: (575)..(655)
197 <400> SEQUENCE: 4
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200 tcaaataatc acagtcattt ggtcaatgtc tatgattaac tcaatgagac aggatgtttg 120
202 gctatagcac caggtacaaa aaatatattt tcatgaagga tcactccctc ttatgtaata 180
204 gatttgggtg agtgagtgag tgagtgagtg catggactca cagcttttgg ctttctgaaa 240
206 taccctgcat cagtcttgtt atgatgattc cttagtgctg ggatggatca tccaggcatt 300
208 taaggtaaca cgatggtaat tctttgctca tttttcaggg aaaaaaaaaa gttatcactt 360
210 ccaaagtcgg catagtcacc cgaagtaaaa aaaaaaaaaa aaaaaaaaag cctcagaggc 420
212 aaaggaaagg ggccgcaacc ttggttaact gtgaaatgac gaatgagaaa actcctcctg 480
214 ctgaagatat tcaggtatat aaaggcacat gaaggaaaac tcaaaacatc attgtcatat 540
216 acacatcttc tggatttttt agcttgcaaa aaaa atg agc acc aaa cct gat atg 595
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         10                  15                  20
ggc acc cta tcc ctg gac tgt aac tta ctg aac gtt cac ctg aga aga   691
Gly Thr Leu Ser Leu Asp Cys Asn Leu Leu Asn Val His Leu Arg Arg
     25                  30                  35
gtc acc tgg caa aat ctg aga cat ctg agt agt atg agc aat tca ttt   739
Val Thr Trp Gln Asn Leu Arg His Leu Ser Ser Met Ser Asn Ser Phe
 40                  45                  50                  55
cct gta gaa tgt cta cga gaa aac ata gct ttt gag ttg ccc caa gag   787
Pro Val Glu Cys Leu Arg Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu
                 60                  65                  70
ttt ctg caa tac acc caa cct atg aag agg gac atc aag aag gcc ttc   835
Phe Leu Gln Tyr Thr Gln Pro Met Lys Arg Asp Ile Lys Lys Ala Phe
             75                  80                  85
tat gaa atg tcc cta cag gcc ttc aac atc ttc agc caa cac acc ttc   883
Tyr Glu Met Ser Leu Gln Ala Phe Asn Ile Phe Ser Gln His Thr Phe
         90                  95                 100
aaa tat tgg aaa gag aga cac ctc aaa caa atc caa ata gga ctt gat   931
Lys Tyr Trp Lys Glu Arg His Leu Lys Gln Ile Gln Ile Gly Leu Asp
     105                 110                 115
cag caa gca gag tac ctg aac caa tgc ttg gag gaa gac gag aat gaa   979
Gln Gln Ala Glu Tyr Leu Asn Gln Cys Leu Glu Glu Asp Glu Asn Glu
 120                 125                 130                 135
aat gaa gac atg aaa gaa atg aaa gag aat gag atg aaa ccc tca gaa   1027
Asn Glu Asp Met Lys Glu Met Lys Glu Asn Glu Met Lys Pro Ser Glu
                 140                 145                 150
gcc agg gtc ccc cag ctg agc agc ctg gaa ctg agg aga tat ttc cac   1075
Ala Arg Val Pro Gln Leu Ser Ser Leu Glu Leu Arg Arg Tyr Phe His
             155                 160                 165
agg ata gac aat ttc ctg aaa gaa aag aaa tac agt gac tgt gcc tgg   1123
Arg Ile Asp Asn Phe Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp
         170                 175                 180
gag att gtc cga gtg gaa atc aga aga tgt ttg tat tac ttt tac aaa   1171
Glu Ile Val Arg Val Glu Ile Arg Arg Cys Leu Tyr Tyr Phe Tyr Lys
     185                 190                 195
ttt aca gct cta ttc agg agg aaa taaggtatat ttttggaatt aaaattcctt  1225
Phe Thr Ala Leu Phe Arg Arg Lys
 200                 205
ttccctccga aatctctttc tccttctcct cctccatctt ctttttaagg attgttgtgc 1285
tgtcctgtaa gcctgtcctc agttggactg gtagcctcgg aacatcaggg acactcacct 1345
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ttaagacatt tttaaaggaa taagattccc tctccgtctt cttctattct ctcttgctct 1465
tttctgtggc cattttgaaa gagctttgct atatatacca cctgtggact tcaccaagac 1525
aatggctaga ggatagggag cagagaatgt tgcaaaatgg taacatttca atgacttaac 1585
tgttttgctg ccaaggttgc ttatcctatg aaaattcagc acattaaaag agcttataca 1645
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290 tttcattact ttaagagtga agatccatag tgaaattgga tggatggttg aattagacga 1825
292 ccattaagct t                                                      1836
295 <210> SEQ ID NO: 5
296 <211> LENGTH: 207
297 <212> TYPE: PRT
298 <213> ORGANISM: Homo sapiens
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305              20                  25                  30
307 Leu Asn Val His Leu Arg Arg Val Thr Trp Gln Asn Leu Arg His Leu
308          35                  40                  45
310 Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu Arg Glu Asn Ile
311      50                  55                  60
313 Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln Pro Met Lys
314  65                  70                  75                  80
316 Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln Ala Phe Asn
317                  85                  90                  95
319 Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg His Leu Lys
320             100                 105                 110
322 Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr Leu Asn Gln Cys
323         115                 120                 125
325 Leu Glu Glu Asp Glu Asn Glu Asn Glu Asp Met Lys Glu Met Lys Glu
326     130                 135                 140
328 Asn Glu Met Lys Pro Ser Glu Ala Arg Val Pro Gln Leu Ser Ser Leu
329 145                 150                 155                 160
331 Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu Lys
332                 165                 170                 175
334 Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Ile Arg Arg
335             180                 185                 190
337 Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Phe Arg Arg Lys
338         195                 200                 205
341 <210> SEQ ID NO: 6
342 <211> LENGTH: 178
343 <212> TYPE: PRT
344 <213> ORGANISM: Homo sapiens
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351              20                  25                  30
353 Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln
354          35                  40                  45
356 Pro Met Lys Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln
357      50                  55                  60
359 Ala Phe Asn Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg
360  65                  70                  75                  80
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